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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: Mon Sep 10 10:45:04 EDT 2007

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Reviewer Comments:

- <220>
- <221> MISC_FEATURE
- <222> (1) .. (1)
- <223> Xaa1 is Mca = (7-methoxycoumarin-4-yl)acetyl

- <220>
- <221> MISC_FEATURE
- <222> (11) .. (11)
- <223> Xaa2 is Dnp = 2,4-dinitrophenyl

- <220>
- <221> MISC_FEATURE
- <222> (12) .. (12)
- <223> Xaa3 is OH

The above "Xaa" responses for sequence id# 12 is invalid, "Xaa" can only represent a single amino acid. Please correct sequence id# 7 and all other remaining sequences with similar errors.

Application No: 10593071 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-28 09:06:28.763
Finished: 2007-08-28 09:06:29.677
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 914 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)

SUBSTITUTE SEQUENCE LISTING

<110> ROUGEOT, Catherine
HUAULME, Jean-Francois
UNGEHEUER, Marie-Noelle
WISNER, Anne
DUFOUR, Evelyne

<120> PEPTIDES DERIVED FROM HUMAN BPLP PROTEIN, POLYNUCLEOTIDES CODING
FOR SAID PEPTIDES AND ANTIBODIES DIRECTED AGAINST SAID PEPTIDES

<130> 296415US0PCT

<140> 10593071
<141> 2007-08-28

<150> PCT/IB05/00700
<151> 2005-03-18

<150> EPO 04290754.3
<151> 2004-03-19

<160> 15

<170> PatentIn version 3.3

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<211> 947
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (81)..(686)

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Met Lys Leu Thr Phe Phe Leu Gly Leu Leu Ala
1 5 10

ctt att tca tgt ttc aca ccc agt gag agt caa aga ttc tcc aga aga 161
Leu Ile Ser Cys Phe Thr Pro Ser Glu Ser Gln Arg Phe Ser Arg Arg
15 20 25

cca tat cta cct ggc cag ctg cca cca cct cca ctc tac agg cca aga 209
Pro Tyr Leu Pro Gly Gln Leu Pro Pro Pro Pro Leu Tyr Arg Pro Arg
30 35 40

tgg gtt cca cca agt ccc cca cct ccc tat gac tca aga ctt aat tca 257
Trp Val Pro Pro Ser Pro Pro Pro Pro Tyr Asp Ser Arg Leu Asn Ser
45 50 55

cca ctt tct ctt ccc ttt gtc cca ggg cga gtt cca cca tct tct ttc 305
Pro Leu Ser Leu Pro Phe Val Pro Gly Arg Val Pro Pro Ser Ser Phe

60	65	70	75	
tct cga ttt agc caa gca gtc att cta tct caa ctc ttt cca ttg gaa				353
Ser Arg Phe Ser Gln Ala Val Ile Leu Ser Gln Leu Phe Pro Leu Glu				
	80	85	90	
tct att aga caa cct cga ctc ttt ccg ggt tat cca aac cta cat ttc				401
Ser Ile Arg Gln Pro Arg Leu Phe Pro Gly Tyr Pro Asn Leu His Phe				
	95	100	105	
cca cta aga cct tac tat gta gga cct att agg ata tta aaa ccc cca				449
Pro Leu Arg Pro Tyr Tyr Val Gly Pro Ile Arg Ile Leu Lys Pro Pro				
	110	115	120	
ttt cct cct att cct ttt ttt ctt gct att tac ctt cct atc tct aac				497
Phe Pro Pro Ile Pro Phe Phe Leu Ala Ile Tyr Leu Pro Ile Ser Asn				
	125	130	135	
cct gag ccc caa ata aac atc acc acc gca gat aca aca atc acc aca				545
Pro Glu Pro Gln Ile Asn Ile Thr Thr Ala Asp Thr Thr Ile Thr Thr				
	140	145	150	155
aat ccc ccc acc act gca aca gca acc acc agg cac ttc cac aaa acc				593
Asn Pro Pro Thr Thr Ala Thr Ala Thr Thr Arg His Phe His Lys Thr				
	160	165	170	
cac aat gac gat cag ctc ctc aac agt acc tat ctc ttc aac acc aga				641
His Asn Asp Asp Gln Leu Leu Asn Ser Thr Tyr Leu Phe Asn Thr Arg				
	175	180	185	
gcc tgc cac ctc cat atc agc agc aac ccc cgc agc atc tac tga				686
Ala Cys His Leu His Ile Ser Ser Asn Pro Arg Ser Ile Tyr				
	190	195	200	
aaatactact caaattctcg ccaaccgtcc tcacacagta ttgctcaatg ccactgtcca				746
agttacgact tccaaccaaa ctatattaag cagcccagcc tttaaaagtt tttggcaaaa				806
actctttgcc atttttgggtt gaacatgcaa taaatgatat tttccaaact gctctgatat				866
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Met Lys Leu Thr Phe Phe Leu Gly Leu Leu Ala Leu Ile Ser Cys Phe			
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Thr Pro Ser Glu Ser Gln Arg Phe Ser Arg Arg Pro Tyr Leu Pro Gly			
20	25	30	

Gln Leu Pro Pro Pro Pro Leu Tyr Arg Pro Arg Trp Val Pro Pro Ser
35 40 45

Pro Pro Pro Pro Tyr Asp Ser Arg Leu Asn Ser Pro Leu Ser Leu Pro
50 55 60

Phe Val Pro Gly Arg Val Pro Pro Ser Ser Phe Ser Arg Phe Ser Gln
65 70 75 80

Ala Val Ile Leu Ser Gln Leu Phe Pro Leu Glu Ser Ile Arg Gln Pro
85 90 95

Arg Leu Phe Pro Gly Tyr Pro Asn Leu His Phe Pro Leu Arg Pro Tyr
100 105 110

Tyr Val Gly Pro Ile Arg Ile Leu Lys Pro Pro Phe Pro Pro Ile Pro
115 120 125

Phe Phe Leu Ala Ile Tyr Leu Pro Ile Ser Asn Pro Glu Pro Gln Ile
130 135 140

Asn Ile Thr Thr Ala Asp Thr Thr Ile Thr Thr Asn Pro Pro Thr Thr
145 150 155 160

Ala Thr Ala Thr Thr Arg His Phe His Lys Thr His Asn Asp Asp Gln
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Ile Ser Ser Asn Pro Arg Ser Ile Tyr
195 200

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<212> PRT
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<400> 3

Gln Arg Phe Ser Arg
1 5

<210> 4
<211> 6
<212> PRT
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<400> 4

Tyr Gln Arg Phe Ser Arg
1 5

<210> 5
<211> 6
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<400> 5

Cys Gln Arg Phe Ser Arg
1 5

<210> 6
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<223> Xaa2 is Gln or Glp when Xaa1 is H. Xaa2 is Gln when Xaa1 is Tyr
or Cys.

<400> 6

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1 5

<210> 7
<211> 5
<212> PRT
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<220>
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<223> Xaa1 is Glp.

<400> 7

Xaa Arg Phe Ser Arg
1 5

<210> 8
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<400> 8

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1 5

<210> 9
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Gln His Asn Pro
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<212> PRT
<213> Homo sapiens

<400> 10

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1 5

<210> 11
<211> 7
<212> PRT
<213> Homo sapiens

<400> 11

Gln Arg Gly Pro Arg Gly Pro
1 5

<210> 12
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa1 is Mca = (7-methoxycoumarin-4-yl)acetyl

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<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa2 is Dnp = 2,4-dinitrophenyl

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa3 is OH

<400> 12

Xaa Arg Pro Pro Gly Phe Ser Ala Phe Lys Xaa Xaa
1 5 10

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa1 is Suc = succinyl

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa5 is Amc = 7-amino-4-methyl coumarin

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Xaa Ala Ala Phe Xaa
1 5

<210> 14

<211> 11

<212> PRT

<213> Homo sapiens

<400> 14

Arg Phe Lys Phe Gln Gln Phe Phe Gly Leu Met
1 5 10

<210> 15

<211> 5

<212> PRT

<213> Homo sapiens

<400> 15

Tyr Gly Gly Phe Met
1 5